

ABSTRACT OF THE DISCLOSURE

The present invention provides methods for identifying evolutionarily significant polynucleotide and polypeptide sequences in human and/or non-human primates which
5 may be associated with a physiological condition, such as enhanced resistance to HCV infection. The invention also provides methods for identifying evolutionarily significant polynucleotides with mutations that are correlated with susceptibility to diseases, such as BRCA1 exon 11. The methods employ comparison of human and non-human primate sequences using statistical methods. Sequences thus identified may be useful as host
10 therapeutic targets and/or in screening assays.

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